CW

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RAW SEQUENCE LISTING   DATE: 04/15/2003
PATENT APPLICATION: US/10/018,445A   TIME: 13:55:39

Input Set : A:\10018445.txt
Output Set: N:\CRF4\04152003\J018445A.raw

```
   4 <110> APPLICANT: C. Frank Bennett
   5        Brett P. Monia
   6        Lex M. Cowsert
   8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 3 EXPRESSION
  10 <130> FILE REFERENCE: RTSP-0211
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/018,445A
C--> 12 <141> CURRENT FILING DATE: 2002-08-09
  12 <150> PRIOR APPLICATION NUMBER: US 09/344,520
  13 <151> PRIOR FILING DATE: 1999-06-25
  15 <160> NUMBER OF SEQ ID NOS: 47
  17 <210> SEQ ID NO: 1
  18 <211> LENGTH: 3170
  19 <212> TYPE: DNA
  20 <213> ORGANISM: Homo sapiens
  22 <220> FEATURE:
  23 <221> NAME/KEY: CDS
  24 <222> LOCATION: (21)..(2387)
  26 <400> SEQUENCE: 1
  27    cgccgcggga ggcggacgag atg cga gcg cgg ccg cgg ccc cgg ccg ctc        50
  28                         Met Arg Ala Arg Pro Arg Pro Arg Pro Leu
  29                          1               5                  10
  31    tgg gtg act gtg ctg gcg ctg ggg gcg ctg gcg ggc gtt ggc gta gga     98
  32    Trp Val Thr Val Leu Ala Leu Gly Ala Leu Ala Gly Val Gly Val Gly
  33                  15                  20                  25
  35    ggg ccc aac atc tgt acc acg cga ggt gtg agc tcc tgc cag cag tgc    146
  36    Gly Pro Asn Ile Cys Thr Thr Arg Gly Val Ser Ser Cys Gln Gln Cys
  37                  30                  35                  40
  39    ctg gct gtg agc ccc atg tgt gcc tgg tgc tct gat gag gcc ctg cct    194
  40    Leu Ala Val Ser Pro Met Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro
  41                  45                  50                  55
  43    ctg ggc tca cct cgc tgt gac ctg aag gag aat ctg ctg aag gat aac    242
  44    Leu Gly Ser Pro Arg Cys Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn
  45            60                  65                  70
  47    tgt gcc cca gaa tcc atc gag ttc cca gtg agt gag gcc cga gta cta    290
  48    Cys Ala Pro Glu Ser Ile Glu Phe Pro Val Ser Glu Ala Arg Val Leu
  49        75                  80                  85                  90
  51    gag gac agg ccc ctc agc gac aag ggc tct gga gac agc tcc cag gtc    338
  52    Glu Asp Arg Pro Leu Ser Asp Lys Gly Ser Gly Asp Ser Ser Gln Val
  53                  95                  100                 105
  55    act caa gtc agt ccc cag agg att gca ctc cgg ctc cgg cca gat gat    386
  56    Thr Gln Val Ser Pro Gln Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp
W--> 57              110                 115                 120
  62    tcg aag aat ttc tcc atc caa gtg cgg cag gtg gag gat tac cct gtg    434
```

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```
       63    Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val
W-->   64        125             130             135
       66    gac atc tac tac ttg atg gac ctg tct tac tcc atg aag gat gat ctg    482
       67    Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu
W-->   68        140             145             150
       70    tgg agc atc cag aac ctg ggt acc aag ctg gcc acc cag atg cga aag    530
       71    Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met Arg Lys
W-->   72    155             160             165             170
       74    ctc acc agt aac ctg cgg att ggc ttc ggg gca ttt gtg gac aag cct    578
       75    Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp Lys Pro
W-->   76                175             180             185
       78    gtg tca cca tac atg tat atc tcc cca cca gag gcc ctc gaa aac ccc    626
       79    Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro
W-->   80            190             195             200
       82    tgc tat gat atg aag acc acc tgc ttg ccc atg ttt ggc tac aaa cac    674
       83    Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His
W-->   84        205             210             215
       86    gtg ctg acg cta act gac cag gtg acc cgc ttc aat gag gaa gtg aag    722
       87    Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu Val Lys
W-->   88        220             225             230
       90    aag cag agt gtg tca cgg aac cga gat gcc cca gag ggt ggc ttt gat    770
       91    Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp
W-->   92    235             240             245             250
       94    gcc atc atg cag gct aca gtc tgt gat gaa aag att ggc tgg agg aat    818
       95    Ala Ile Met Gln Ala Thr Val Cys Asp Glu Lys Ile Gly Trp Arg Asn
W-->   96                255             260             265
       98    gat gca tcc cac ttg ctg gtg ttt acc act gat gcc aag act cat ata    866
       99    Asp Ala Ser His Leu Leu Val Phe Thr Thr Asp Ala Lys Thr His Ile
W-->   100               270             275             280
      102    gca ttg gac gga agg ctg gca ggc att gtc cag cct aat gac ggg cag    914
      103    Ala Leu Asp Gly Arg Leu Ala Gly Ile Val Gln Pro Asn Asp Gly Gln
W-->   104       285             290             295
      106    tgt cat gtt ggt agt gac aat cat tac tct gcc tcc act acc atg gat    962
      107    Cys His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr Met Asp
W-->   108       300             305             310
      110    tat ccc tct ttg ggg ctg atg act gag aag cta tcc cag aaa aac atc   1010
      111    Tyr Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln Lys Asn Ile
W-->   112       315             320             325             330
      114    aat ttg atc ttt gca gtg act gaa aat gta gtc aat ctc tat cag aac   1058
      115    Asn Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr Gln Asn
W-->   116               335             340             345
      118    tat agt gag ctc atc cca ggg acc aca gtt ggg gtt ctg tcc atg gat   1106
      119    Tyr Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser Met Asp
W-->   120       350             355             360
      122    tcc agc aat gtc ctc cag ctc att gtt gat gct tat ggg aaa atc cgt   1154
      123    Ser Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg
W-->   124       365             370             375
      126    tct aaa gtc gag ctg gaa gtg cgt gac ctc cct gaa gag ttg tct cta   1202
      127    Ser Lys Val Glu Leu Glu Val Arg Asp Leu Pro Glu Glu Leu Ser Leu
```

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```
W--> 128        380                385                390
     130    tcc ttc aat gcc acc tgc ctc aac aat gag gtc atc cct ggc ctc aag    1250
     131    Ser Phe Asn Ala Thr Cys Leu Asn Asn Glu Val Ile Pro Gly Leu Lys
W--> 132        395                400                405                410
     134    tct tgt atg gga ctc aag att gga gac acg gtg agc ttc agc att gag    1298
     135    Ser Cys Met Gly Leu Lys Ile Gly Asp Thr Val Ser Phe Ser Ile Glu
W--> 136                 415                420                425
     138    gcc aag gtg cga ggc tgt ccc cag gag aag gag aag tcc ttt acc ata    1346
     139    Ala Lys Val Arg Gly Cys Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile
W--> 140                 430                435                440
     142    aag ccc gtg ggc ttc aag gac agc ctg atc gtc cag gtc acc ttt gat    1394
     143    Lys Pro Val Gly Phe Lys Asp Ser Leu Ile Val Gln Val Thr Phe Asp
W--> 144        445                450                455
     146    tgt gac tgt gcc tgc cag gcc caa gct gaa cct aat agc cat cgc tgc    1442
     147    Cys Asp Cys Ala Cys Gln Ala Gln Ala Glu Pro Asn Ser His Arg Cys
W--> 148        460                465                470
     150    aac aat ggc aat ggg acc ttt gag tgt ggg gta tgc cgt tgt ggg cct    1490
     151    Asn Asn Gly Asn Gly Thr Phe Glu Cys Gly Val Cys Arg Cys Gly Pro
W--> 152        475                480                485                490
     154    ggc tgg ctg gga tcc cag tgt gag tgc tca gag gag gac tat cgc cct    1538
     155    Gly Trp Leu Gly Ser Gln Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro
W--> 156                 495                500                505
     158    tcc cag cag gac gag tgc agc ccc cga gag ggt cag ccc gtc tgc agc    1586
     159    Ser Gln Gln Asp Glu Cys Ser Pro Arg Glu Gly Gln Pro Val Cys Ser
W--> 160                 510                515                520
     162    cag cgg ggc gag tgc ctc tgt ggt caa tgt gtc tgc cac agc agt gac    1634
     163    Gln Arg Gly Glu Cys Leu Cys Gly Gln Cys Val Cys His Ser Ser Asp
W--> 164                 525                530                535
     166    ttt ggc aag atc acg ggc aag tac tgc gag tgt gac gac ttc tcc tgt    1682
     167    Phe Gly Lys Ile Thr Gly Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys
W--> 168        540                545                550
     170    gtc cgc tac aag ggg gag atg tgc tca ggc cat ggc cag tgc agc tgt    1730
     171    Val Arg Tyr Lys Gly Glu Met Cys Ser Gly His Gly Gln Cys Ser Cys
W--> 172    555                560                565                570
     174    ggg gac tgc ctg tgt gac tcc gac tgg acc ggc tac tac tgc aac tgt    1778
     175    Gly Asp Cys Leu Cys Asp Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys
W--> 176                 575                580                585
     178    acc acg cgt act gac acc tgc atg tcc agc aat ggg ctg ctg tgc agc    1826
     179    Thr Thr Arg Thr Asp Thr Cys Met Ser Ser Asn Gly Leu Leu Cys Ser
W--> 180                 590                595                600
     182    ggc cgc ggc aag tgt gaa tgt ggc agc tgt gtc tgt atc cag ccg ggc    1874
     183    Gly Arg Gly Lys Cys Glu Cys Gly Ser Cys Val Cys Ile Gln Pro Gly
W--> 184                 605                610                615
     186    tcc tat ggg gac acc tgt gag aag tgc ccc acc tgc cca gat gcc tgc    1922
     187    Ser Tyr Gly Asp Thr Cys Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys
W--> 188        620                625                630
     190    acc ttt aag aaa gaa tgt gtg gag tgt aag aag ttt gac cgg gag ccc    1970
     191    Thr Phe Lys Lys Glu Cys Val Glu Cys Lys Lys Phe Asp Arg Glu Pro
W--> 192        635                640                645                650
```

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Input Set : **A:\10018445.txt**
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```
      194      tac atg acc gaa aat acc tgc aac cgt tac tgc cgt gac gag att gag      2018
      195      Tyr Met Thr Glu Asn Thr Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu
W--> 196                  655                 660                 665
      198      tca gtg aaa gag ctt aag gac act ggc aag gat gca gtg aat tgt acc      2066
      199      Ser Val Lys Glu Leu Lys Asp Thr Gly Lys Asp Ala Val Asn Cys Thr
W--> 200                  670                 675                 680
      202      tat aag aat gag gat gac tgt gtc gtc aga ttc cag tac tat gaa gat      2114
      203      Tyr Lys Asn Glu Asp Asp Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp
W--> 204                  685                 690                 695
      206      tct agt gga aag tcc atc ctg tat gtg gta gaa gag cca gag tgt ccc      2162
      207      Ser Ser Gly Lys Ser Ile Leu Tyr Val Val Glu Glu Pro Glu Cys Pro
W--> 208            700                 705                 710
      210      aag ggc cct gac atc ctg gtg gtc ctg ctc tca gtg atg ggg gcc att      2210
      211      Lys Gly Pro Asp Ile Leu Val Val Leu Leu Ser Val Met Gly Ala Ile
W--> 212      715                 720                 725                 730
      214      ctg ctc att ggc ctt gcc gcc ctg ctc atc tgg aaa ctc ctc atc acc      2258
      215      Leu Leu Ile Gly Leu Ala Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr
W--> 216                  735                 740                 745
      218      atc cac gac cga aaa gaa ttc gct aaa ttt gag gaa gaa cgc gcc aga      2306
      219      Ile His Asp Arg Lys Glu Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg
W--> 220                  750                 755                 760
      222      gca aaa tgg gac aca gcc aac aac cca ctg tat aaa gag gcc acg tct      2354
      223      Ala Lys Trp Asp Thr Ala Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser
W--> 224                  765                 770                 775
      226      acc ttc acc aat atc acg tac cgg ggc act taa tgataagcag tcatcctcag  2407
      227      Thr Phe Thr Asn Ile Thr Tyr Arg Gly Thr
W--> 228            780                 785
      230      atcattatca gcctgtgcca ggattgcagg agtccctgcc atcatgttta cagaggacag  2467
      232      tatttgtggg gagggatttc ggggctcaga gtggggtagg ttgggagaat gtcagtatgt  2527
      234      ggaagtgtgg gtctgtgtgt gtgtatgtgg gggtctgtgt gtttatgtgt gtgtgttgtg  2587
      236      tgtgggagtg tgtaatttaa aattgtgatg tgtcctgata agctgagctc cttagccttt  2647
      238      gtcccagaat gcctcctgca gggattcttc ctgcttagct tgagggtgac tatggagctg  2707
      240      agcaggtgtt cttcattacc tcagtgagaa gccagctttc ctcatcaggc cattgtccct  2767
      242      gaagagaagg gcagggctga ggcctctcat tccagaggaa gggacaccaa gccttggctc  2827
      244      taccctgagt tcataaattt atggttctca ggcctgactc tcagcagcta tggtaggaac  2887
      246      tgctggcttg gcagcccggg tcatctgtac ctctgcctcc tttcccctcc ctcaggccga  2947
      248      aggaggagtc agggagagct gaactattag agctgcctgt gccttttgcc atcccctcaa  3007
      250      cccagctatg gttctctcgc aagggaagtc cttgcaagct aattctttga cctgttggga  3067
      252      gtgaggatgt ctgggccact caggggtcat tcatggcctg ggggatgtac cagcatctcc  3127
      254      cagttcataa tcacaaccct tcagatttgc cttattggca gcg                     3170
      257 <210> SEQ ID.NO: 2
      258 <211> LENGTH: 23
      259 <212> TYPE: DNA
      260 <213> ORGANISM: Artificial Sequence
      262 <220> FEATURE:
      263 <223> OTHER INFORMATION: PCR Primer
      265 <400> SEQUENCE: 2
      266     tttaccactg atgccaagac tca                                           23
      269 <210> SEQ ID NO: 3
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PATENT APPLICATION: **US/10/018,445A**   TIME: 13:55:39

Input Set : **A:\10018445.txt**
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```
270 <211> LENGTH: 21
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: PCR Primer
277 <400> SEQUENCE: 3
278    ccgtcattag gctggacaat g                              21
281 <210> SEQ ID NO: 4
282 <211> LENGTH: 25
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: PCR Probe
289 <400> SEQUENCE: 4
290    atagcattgg acggaaggct ggcag                          25
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 19
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: PCR Primer
301 <400> SEQUENCE: 5
302    gaaggtgaag gtcggagtc                                 19
305 <210> SEQ ID NO: 6
306 <211> LENGTH: 20
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: PCR Primer
313 <400> SEQUENCE: 6
314    gaagatggtg atgggatttc                                20
317 <210> SEQ ID NO: 7
318 <211> LENGTH: 20
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: PCR Probe
325 <400> SEQUENCE: 7
326    caagcttccc gttctcagcc                                20
329 <210> SEQ ID NO: 8
330 <211> LENGTH: 18
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Antisense Oligonucleotide
337 <400> SEQUENCE: 8
338    gcatctcgtc cgcctccc                                  18
341 <210> SEQ ID NO: 9
342 <211> LENGTH: 18
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/018,445A**

DATE: 04/15/2003
TIME: 13:55:40

Input Set : **A:\10018445.txt**
Output Set: **N:\CRF4\04152003\J018445A.raw**

```
L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:140 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:152 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:184 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:196 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:200 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:208 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:212 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:224 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
```